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TECH CENTER 1600/2808

(1) GENERAL INFORMATION

- (i) APPLICANT: Hadlaczky, Gyula
Szalay, Aladar
- (ii) TITLE OF THE INVENTION: ARTIFICIAL CHROMOSOMES, USES THEREOF
AND METHODS FOR PREPARING ARTIFICIAL CHROMOSOMES
- (iii) NUMBER OF SEQUENCES: 34
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Heller Ehrman White & McAuliffe
(B) STREET: 4250 Executive Square, 7th Floor
(C) CITY: La Jolla
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 92037
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US/09/724,693
(B) FILING DATE: 28-NOV-2000
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/835,682
(B) FILING DATE: 10-APR-1997
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/695,191
(B) FILING DATE: 07-AUG-1996
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/682,080
(B) FILING DATE: 15-JUL-1996
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/629,822
(B) FILING DATE: 10-APR-1996
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Seidman, Stephanie L
(B) REGISTRATION NUMBER: 33,779
(C) REFERENCE/DOCKET NUMBER: 24601-402G
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 858-450-8403
(B) TELEFAX: 858-587-5360
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1293 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GAATTCATCA	TTTTTCANGT	CCTCAAGTGG	ATGTTTCTCA	TTTNCATGA	TTTTAAGTTT	60
TCTCGCCATA	TTCTGGTCC	TACAGTGTGC	ATTTCTCCAT	TTNCACGTT	TTNCAGTGAT	120
TTCGTCATTT	TCAAGTCCTC	AAGTGGATGT	TTCTCATTTN	CCATGAATTT	CAGTTTTCTN	180
GCCATATTCC	ACGTCCTACA	GNGGACATTT	CTAAATTTNC	CACCTTTTTT	AGTTTTCCCTC	240
GCCATATTTT	ACGTCCTAAA	ATGTGTATTT	CTCGTTTNCC	GTGATTTTCA	GTTTTCTCGC	300
CAGATTCCAG	GTCCTATAAT	GTGCATTTCT	CATTTNNCAC	GTTTTTCAGT	GATTTTCGTCA	360
TTTTTTCAAG	TCGGCAAGTG	GATGTTTCTC	ATTTNCCATG	ATTTNCAGTT	TTCTTGNAAT	420
ATTCATGTGC	CTACAATGAT	CATTTTAAAT	TTTCCACCTT	TTCAATTTTC	CACGCCATAT	480
TTTATGTCTT	AAAGTGTATA	TTTCTCCTTT	TCCGCGATTT	TCAGTTTCTT	CGCCATATTC	540
CAGGTCCTAC	AGTGTGCATT	CCTCATTTT	CACCTTTTTT	ACTGATTTCT	TCATTTTTC	600
AGTCGTCAAC	TGGATCTTTC	TAATTTTCCA	TGATTTTTCAG	TTATCTTGTC	ATATTTCCATG	660
TCCTACAGTG	GACATTTCTA	AATTTTCCAA	CTTTTTCAT	TTTTCTCGAC	ATATTTGACG	720
TGCTAAAGTG	TGTATTTCTT	ATTTTCCGTG	ATTTTCAGTT	TTCTCGCCAT	ATTTCCAGGTC	780
CTAATAGTGT	GCATTTCTCA	TTTTTCACGT	TTTTTCAGTGA	TTTCGTCAAT	TTTTCCAGTT	840
GTCAAGGGGA	TGTTTCTCAT	TTTCCATGAG	TGTCAGTTT	CTTGCTATAT	TCCATGTCTT	900
ACAGTGACAT	TTCTAAATAT	TATACCTTTT	TCAGTTTTT	TCACCATATT	TCACGTCCTA	960
AAGTATATAT	TTCTCATTTT	CCCTGATTTT	CAGTTTCCTT	GCCATATTCC	AGGTCCTACA	1020
GTGTGCATTT	CTCATTTTTC	ACGTTTTTCA	GTAATTTCTT	CATTTTAA	GCCCTCAAAT	1080
GGATGTTTCT	CATTTTCCAT	GATTTTCAGT	TTTCTTGCCA	TATACCATGT	CCTACAGTGG	1140
ACATTTCTAA	ATTATCCACC	TTTTTCAGTT	TTTCATCGGC	ACATTTACAG	TCCTAAAGTG	1200
TGTATTTCTA	ATTTTCAGTG	ATTTTCAGTT	TTCTCGCCAT	ATTCCAGGAC	CTACAGTGTG	1260
CATTTCTCAT	TTTTTCACGT	TTTCAGTGAA	TTT			1293

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1044 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGGCCTATGG	TGAAAAAGGA	AATATCTTCC	CCTGAAAACT	AGACAGAAGG	ATTCTCAGAA	60
TCTTATTTGT	GATGTGCGCC	CCTCAACTAA	CAGTGTGAA	GCTTTCTTTT	GATAGAGCAG	120
TTTTGAAACA	CTCTTTTGT	AAAATCTGCA	AGAGGATATT	TGGATAGCTT	TGAGGATTTT	180
CGTTGGAAAC	GGGATTGTCT	TCATATAAAC	CCTAGACAGA	AGCATTCTCA	GAAGCTTCAT	240
TGGGATGTTT	CAGTTGAAGT	CACAGTGTTG	AACAGTCCCC	TTTCATAGAG	CAGGTTTGAA	300
ACACTCTTTT	TTGTAGTATC	TGGAAGTGGA	CATTTGGAGC	GATCTCAGGA	CTGCGGTGAA	360
AAAGGAAATA	TCTTCCAATA	AAAGCTAGAT	AGAGGCAATG	TCAGAAACCT	TTTTCATGAT	420
GTATCTACTC	AGCTAACAGA	GTTGAACCTT	CCTTTGAGAG	AGCAGTTTTG	AAACACTCTT	480
TTTGTGGAAT	CTGCAAGTGG	ATATTTGTCT	AGCTTTGAGG	ATTTTCGTTG	GAAACGGGAT	540
TACATATAAA	AAGCAGACAG	CAGCATTTCC	AGAAACTTCT	TTGTGATGTT	TGCATTCAAG	600
TCACAGAGTT	GAACATTCCC	TTTCATAGAG	CAGGTTTGAA	ACACACTTTT	TGATGTATCT	660
GGATGTGGAC	ATTTGCAGCG	CTTTCAGGCC	TAAGGTGAAA	AGGAAATATC	TTCCCCTGAA	720
AACTAGACAG	AAGCATTTCT	AGAAACTTAT	TTGTGATGTT	CGCCCTCAAC	TAACAGTGTT	780
GAAGCTTTCT	TTTGATAGAG	GCAGTTTTGA	AACACTCTTT	TGTGGAATCT	GCAAGTGGAT	840
ATTTGTCTAG	CTTTGAGGAT	TTCTTTGGAA	ACGGGATTAC	ATATAAAAAG	CAGACAGCAG	900

CATTCCCAGA	ATCTTGTGTTG	TGATGTTTGC	ATTCAAGTCA	CAGAGTTGAA	CATTCCCTTT	960
CAGAGAGCAG	GTTTGAACAC	TCTTTTATA	GTATCTGGAT	GTGGACATTT	GGAGCGCTTT	1020
CAGGGGGGAT	CCTCTAGAAT	TCCT				1044

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2492 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Q1

CTGCAGCTGG	GGGTCTCCAA	TCAGGCAGGG	CCCCCTTACT	ACTCAGATGG	GGTGGCCGAG	60
TAGGGGAAGG	GGGTGCAGGC	TGCATGAGTG	GACACAGCTG	TAGGACTACC	TGGGGGCTGT	120
GGATCTATGG	GGGTGGGGAG	AAGCCCAGTG	ACAGTGCCTA	GAAGAGACAA	GGTGGCCTGA	180
GAGGGTCTGA	GGAACATAGA	GCTGGCCATG	TTGGGGCCAG	GTCTCAAGCA	GGAAAGTGAGG	240
AATGGGACAG	GCTTGAGGAT	ACTTACTCTA	GTAGCCAGGA	TAGCAAGGAG	GGCTTGGGGT	300
TGCTATCCTG	GGGTTCAACC	CCCCAGGTTG	AAGGCCCTGG	GGGAGATGGT	CCCAGGACAT	360
ATTACAATGG	ACACAGGAGG	TTGGGACACC	TGGAGTCACC	AAACAAAACC	ATGCCAAGAG	420
AGACCATGAG	TAGGGGTGTC	CAGTCCAGCC	CTCTGACTGA	GCTGCATTGT	TCAAATCCAA	480
AGGGCCCCCTG	CTGCCACCTA	GTGGCTGATG	GCATCCACAT	GACCCTGGGC	CACACGCGTT	540
TAGGGTCTCT	GTGAAGACCA	AGATCCTTGT	TACATTGAAC	GACTCCTAAA	TGAGCAGAGA	600
TTTCCACCTA	TTCGAAACAA	TCACATAAAA	TCCATCCTGG	AAAAAGCCTG	GGGGATGGCA	660
CTAAGGCTAG	GGATAGGGTG	GGATGAAGAT	TATAGTTACA	GTAAGGGGTT	TAGGGTTAGG	720
GATCAACGTT	GGTTAGGAGT	TAGGGATACA	GTAGGGTACC	GGTAGGGTTA	GGGGTTAGGG	780
TTAGGGGTTA	GGGTTAGGGT	TAGGGTTAGG	GTTAGGGTTA	GGGGTTAGGG	GTTAGGGTTA	840
GGGTTAGGTT	TTGGGGTGGC	GTATTTTGGT	CTTATACGCT	GTGTTCCACT	GGCAATGAAA	900
AGAGTTCTTG	TTTTTCCTTC	AGCAATTTGT	CATTTTAAAT	AGAGTTTAGC	AATTCTAACA	960
GATATAGACC	AGCTGTGCTA	TCTCATTGTG	GTTTTCAATT	GTAACCACAT	TGTGGTTTCA	1020
ATGTGTTTAC	TTGCCATCTG	TAGATCTTCT	TTGCGTGAGG	TGTCTGTTCA	GATGTGTGTG	1080
CATTCTCTGN	NTTTNGGCTG	TTTAACTTAT	TGTTTAGTTT	TAATAATTTT	TTATATATTT	1140
GAAGACAAAT	CTTTCTCAGA	TGTGTATTTG	CAAATATTTT	TTCAATATGA	GGCTTGCTTT	1200
TGTCTCTAAC	AAGGTCTCTT	CAGAGATAAC	TTAAATATAA	GAAATCCACA	CTGTCACTTC	1260
TTTTGTGTAT	ATCTACCTTT	TGTGTCATTT	GTTAAATTC	ATTACCAAAC	CCAAAGGCAG	1320
ATAGCTTTTC	TTCTATTGTT	TCTTCTAGAA	ATTTGTATAG	TTTTGCATTT	TTAGTGTAAG	1380
GATGATTTTG	AGTGATTATT	TGTGTAAGTT	GTTAAAGTTT	CGTCTATATC	CATATCATTT	1440
CTTATGGTTT	CCAATTAATC	GTTCCCTCAC	TATTTTGGG	AAAGACACAG	GATAGTGGGC	1500
TTTGTTAGAG	TAGATAGGTA	GCTAGACATG	AACAGGAGGG	GGCCTCCTGG	AAAAGGGAAA	1560
GTCTGGGAAG	GCTCACCTGG	AGGACCACCA	AAAATTCACA	TATTAGTAGC	ATCTCTAGTG	1620
CTGGAGTGGA	TGGGCACTTG	TCAATTGTGG	GTAGGAGGGA	AAAGAGGTCC	TATGCAGAAA	1680
GAAACTCCCT	AGAACTCCTC	TGAAGATGCC	CCAATCATTC	ACTCTGCAAT	AAAAATGTCA	1740
GAATATTGCT	AGCTACATGC	TGATAAGGNN	AAAGGGGACA	TTCTTAAGTG	AAACCTGGCA	1800
CCATAAGTAC	AGATTAGGGC	AGAGAAGGAC	ATTCAAAGA	GGCAGGCGCA	GTAGGTACAA	1860
ACGTGATCGC	TGTCAGTGTG	CCTGGGATGG	CGGGAAGGAG	GCTGGTGCCA	GAGTGGATTG	1920
GTATTGATCA	CCACACATAT	ACCTCAACCA	ACAGTGAGGA	GGTCCCACAA	GCCTAAGTGG	1980
GGCAAGTTGG	GGAGCTAAGG	CAGTAGCAGG	AAAACCAGAC	AAAGAAAACA	GGTGGAGACT	2040
TGAGACAGAG	GCAGGAATGT	GAAGAAATCC	AAAATAAAAT	TCCCTGCACA	GGACTCTTAG	2100
GCTGTTTAAT	GCATCGCTCA	GTCCCACTCC	TCCCTATTTT	TCTACAATAA	ACTCTTTACA	2160
CTGTGTTTCT	TTTCAATGAA	GTTATCTGCC	ATCTTTGTAT	TGCCTCTTGG	TGAAAATGTT	2220
TCTTCCAAGT	TAAACAAGAA	CTGGGACATC	AGCTCTCCCC	AGTAATAGCT	CCGTTTCAGT	2280
TTGAATTTAC	AGAAGTATG	GGCTTAATAA	CTGGCGCTCT	GACTTTAGTG	GTGCAGGAGG	2340
CCGTACACAC	GGGACCAAGA	GTGCCCTGCC	TAGTCCCCAT	CTGCCCGCAG	GTGGCGGCTG	2400
CCTCGACACT	GACAGCAATA	GGGTCCGGCA	GTGTCCCCAG	CTGCCAGCAG	GGGGCGTACG	2460
ACGACTACAC	TGTGAGCAAG	AGGGCCCTGC	AG			2492

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGGGAATTCA TTGGGATGTT TCAGTTGA

28

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGAAAGTCCC CCCTAGGAGA TCTTAAGGA

29

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 47 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCGCTTAATA CTCTGATGAG TCCGTGAGGA CGAAACGCTC TCGCACC

47

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGATTTTAAAT TAATTAAGCC CGGGC

25

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:
(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TAAATTTAAT TAATTCGGGC CCGTCGA

27

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(D) OTHER INFORMATION IL-2 signal sequence

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TAC AGG ATG CAA CTC CTG TCT TGC ATT GCA CTA AGT CTT GCA CTT
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu

48

GTC ACA AAC AGT GCA CCT ACT
Val Thr Asn Ser Ala Pro Thr

69

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 945 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 1...942
(D) OTHER INFORMATION: Renilla Reinformis Luciferase

(x) PUBLICATION INFORMATION:

(H) Document Number: 5,418,155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGC TTA AAG ATG ACT TCG AAA GTT TAT GAT CCA GAA CAA AGG AAA CGG 48
Ser Leu Lys Met Thr Ser Lys Val Tyr Asp Pro Glu Gln Arg Lys Arg
1 5 10 15

ATG ATA ACT GGT CCG CAG TGG TGG GCC AGA TGT AAA CAA ATG AAT GTT 96
Met Ile Thr Gly Pro Gln Trp Trp Ala Arg Cys Lys Gln Met Asn Val
20 25 30

CTT GAT TCA TTT ATT AAT TAT TAT GAT TCA GAA AAA CAT GCA GAA AAT 144
Leu Asp Ser Phe Ile Asn Tyr Tyr Asp Ser Glu Lys His Ala Glu Asn
35 40 45

GCT GTT ATT TTT TTA CAT GGT AAC GCG GCC TCT TCT TAT TTA TGG CGA 192
Ala Val Ile Phe Leu His Gly Asn Ala Ala Ser Ser Tyr Leu Trp Arg
50 55 60

CAT GTT GTG CCA CAT ATT GAG CCA GTA GCG CGG TGT ATT ATA CCA GAT 240
His Val Val Pro His Ile Glu Pro Val Ala Arg Cys Ile Ile Pro Asp
65 70 75 80

CTT ATT GGT ATG GGC AAA TCA GGC AAA TCT GGT AAT GGT TCT TAT AGG 288
Leu Ile Gly Met Gly Lys Ser Gly Lys Ser Gly Asn Gly Ser Tyr Arg
85 90 95

TTA CTT GAT CAT TAC AAA TAT CTT ACT GCA TGG TTG AAC TTC TTA ATT 336
Leu Leu Asp His Tyr Lys Tyr Leu Thr Ala Trp Leu Asn Phe Leu Ile
100 105 110

TAC CAA AGA AGA TCA TTT TTT GTC GGC CAT GAT TGG GGT GCT TGT TTG 384
Tyr Gln Arg Arg Ser Phe Phe Val Gly His Asp Trp Gly Ala Cys Leu
115 120 125

GCA TTT CAT TAT AGC TAT GAG CAT CAA GAT AAG ATC AAA GCA ATA GTT 432
Ala Phe His Tyr Ser Tyr Glu His Gln Asp Lys Ile Lys Ala Ile Val
130 135 140

CAC GCT GAA AGT GTA GTA GAT GTG ATT GAA TCA TGG GAT GAA TGG CCT 480
His Ala Glu Ser Val Val Asp Val Ile Glu Ser Trp Asp Glu Trp Pro
145 150 155 160

GAT ATT GAA GAA GAT ATT GCG TTG ATC AAA TCT GAA GAA GGA GAA AAA 528
Asp Ile Glu Glu Asp Ile Ala Leu Ile Lys Ser Glu Glu Gly Glu Lys
165 170 175

ATG GTT TTG GAG AAT AAC TTC TTC GTG GAA ACC ATG TTG CCA TCA AAA 576
Met Val Leu Glu Asn Asn Phe Phe Val Glu Thr Met Leu Pro Ser Lys
180 185 190

ATC ATG AGA AAG TTA GAA CCA GAA GAA TTT GCA GCA TAT CTT GAA CCA 624
Ile Met Arg Lys Leu Glu Pro Glu Glu Phe Ala Ala Tyr Leu Glu Pro
195 200 205

TTC AAA GAG AAA GGT GAA GTT CGT CGT CCA ACA TTA TCA TGG CCT CGT 672
Phe Lys Glu Lys Gly Glu Val Arg Arg Pro Thr Leu Ser Trp Pro Arg
210 215 220

GAA ATC CCG TTA GTA AAA GGT GGT AAA CCT GAC GTT GTA CAA ATT GTT 720
Glu Ile Pro Leu Val Lys Gly Gly Lys Pro Asp Val Val Gln Ile Val
225 230 235 240

AGG AAT TAT AAT GCT TAT CTA CGT GCA AGT GAT GAT TTA CCA AAA ATG 768

Arg	Asn	Tyr	Asn	Ala	Tyr	Leu	Arg	Ala	Ser	Asp	Asp	Leu	Pro	Lys	Met	
				245					250					255		
TTT	ATT	GAA	TCG	GAT	CCA	GGA	TTC	TTT	TCC	AAT	GCT	ATT	GTT	GAA	GGC	816
Phe	Ile	Glu	Ser	Asp	Pro	Gly	Phe	Phe	Ser	Asn	Ala	Ile	Val	Glu	Gly	
			260				265					270				
GCC	AAG	AAG	TTT	CCT	AAT	ACT	GAA	TTT	GTC	AAA	GTA	AAA	GGT	CTT	CAT	864
Ala	Lys	Lys	Phe	Pro	Asn	Thr	Glu	Phe	Val	Lys	Val	Lys	Gly	Leu	His	
		275					280					285				
TTT	TCG	CAA	GAA	GAT	GCA	CCT	GAT	GAA	ATG	GGA	AAA	TAT	ATC	AAA	TCG	912
Phe	Ser	Gln	Glu	Asp	Ala	Pro	Asp	Glu	Met	Gly	Lys	Tyr	Ile	Lys	Ser	
	290					295					300					
TTC	GTT	GAG	CGA	GTT	CTC	AAA	AAT	GAA	CAA	TAA						945
Phe	Val	Glu	Arg	Val	Leu	Lys	Asn	Glu	Gln							
305						310										

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTGAATTC A TGTACAGGAT GCAACTCCTG 30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGAATTCA GTAGGTGCAC TGTTTGTAC 30

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAACTG	GGTTTGCCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAC	GACTGACACC	ATTAACACTT	TGTCAGCCTC	AGTGACTACA	GTCATAGATG	240
AACAGGCCTC	AGCTAATGTC	AAGATACAGA	GAGGTCTCAT	GCTGGTTAAT	CAACTCATAG	300
ATCTTGTCCA	GATACAACCTA	GATGTATTAT	GACAAATAAC	TCAGCAGGGA	TGTGAACAAA	360
AGTTTCCGGG	ATTGTGTGTT	ATTTCCATT	AGTATGTTAA	ATTTACTAGG	ACAGCTAATT	420
TGTCAAAAAG	TCTTTTTCAG	TATATGTTAC	AGAATTGGAT	GGCTGAATTT	GAACAGATCC	480
TTCGGGAATT	GAGACTTCAG	GTCAACTCCA	CGCGCTTGGG	CCTGTCGCTG	ACCAAAGGAT	540
TACCCAATTG	GATCTCCTCA	GCATTTTCTT	TCTTTAAAAA	ATGGGTGGGA	TTAATATTAT	600
TTGGAGATAC	ACTTTGCTGT	GGATTAGTGT	TGCTTCTTTG	ATTGGTCTGT	AAGCTTAAGG	660
CCCCAACTAG	GAGAGACAAG	GTGGTTATTG	CCCAGGCGCT	TGCAGGACTA	GAACATGGAG	720
CTTCCCCTGA	TATATGGTTA	TCTATGCTTA	GGCAATAGGT	CGCTGGCCAC	TCAGCTCTTA	780
TATCCCACGA	GGCTAGTCTC	ATTGTACGGG	ATAGAGTGAG	TGTGCTTCAG	CAGCCCCGAG	840
GAGTTGCAAG	GCTAAGCACT	GCAATGGAAA	GGCTCTGCGG	CATATATGTG	CCTATTCTAG	900
GGGGACATGT	CATCTTTCAT	GAAGGTTTCT	TGTCCTAGTT	CCCTTCCCCC	AGGCAAAACG	960
ACACGGGAGC	AGGTCAGGGT	TGCTCTGGGT	AAAAGCCTGT	GAGCCTGGGA	GCTAATCCTG	1020
TACATGGCTC	CTTTACCTAC	ACACTGGGGA	TTTGACCTCT	ATCTCCACTC	TCATTAATAT	1080
GGGTGGCCTA	TTTGCTCTTA	TTAAAAGGAA	AGGGGGAGAT	GTTGGGAGCC	GCGCCACAT	1140
TCGCCGTTAC	AAGATGGCGC	TGACAGCTGT	GTTCTAAGTG	GTAACAAAT	AATCTGCGCA	1200
TGTGCCGAGG	GTGGTCTTTC	ACTCCATGTG	CTCTGCCTTC	CCCGTGACGT	CAACTCGGCC	1260
GATGGGCTGC	AGCCAATCAG	GGAGTGACAC	GTCTTAGGCG	AAGGAGAATT	CTCCTTAATA	1320
GGGACGGGGT	TTCGTTCTCT	CTCTCTCTCT	TCTTCTCTCT	TCGCTCTCTT	TCGCTCTCTT	1380
GCTTCCCCTA	AAGTGATAAT	GATTATCATC	TACATATCAC	AACGTGCGTG	GAGG	1434

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	AGAGCAGCGT	TGGGGGATAA	60
TGTCGACATT	TCCACTCCCA	ATGACGGTGA	TGTATAATGC	TCAAGTATTC	TCCTGCTTTT	120
TTACCACTAA	CTAGGAACTG	GGTTTGCCCT	TAATTCAGAC	AGCCTTGGCT	CTGTCTGGAC	180
AGGTCCAGAT	ACAACCTAGAT	GTATTATGAC	AAATAACTCA	GCAGGGATGT	GAACAAAAGT	240
TTCCGGGATT	GCGTGTTATT	TCCATCCAGT	ATGTTAAATT	TACTAGGGCA	GCTAATTTGT	300
CAAAAAGTCT	TTTCCAGTAT	ATGTTACAGA	ATTGGATGGC	TGAATTTGAA	CAGATCCTTC	360
GGGAATTGAG	ACTTCAGGTC	AACTCCACGC	GCTTGGACCT	GTCCCTGACC	AAAGGATTAC	420
CCAATTGGAT	CTCCTCAGCA	TTTCTTTTCT	TTAAAAAATG	GGTGGGATTA	ATATTATTTG	480
GAGATACACT	TTGCTGTGGA	TTAGTGTTC	TTCTTTGATT	GGTCTGTAAG	CTTAAGGCCC	540
AAACTAGGAG	AGACAAGGTG	GTTATTGCCC	AGGCGCTTGC	AGGACTAGAA	CATGGAGCTT	600
CCCCTGATAT	ATCTATGCTT	AGGCAATAGG	TCGCTGGCCA	CTCAGCTCTT	ATATCCCATG	660
AGGCTAGTCT	CATTGCACGG	GATAGAGTGA	GTGTGCTTCA	GCAGCCCGAG	AGAGTTGCAC	720
GGCTAAGCAC	TGCAATGGAA	AGGCTCTGCG	GCATATATGA	GCCTATTCTA	GGGAGACATG	780
TCATCTTTCA	AGAAGGTTGA	GTGTCCAAGT	GTCTTCTCTC	CAGGCAAAAC	GACACGGGAG	840
CAGGTACAGG	TTGCTCTGGG	TAAAAGCCTG	TGAGCCTAAG	AGCTAATCCT	GTACATGGCT	900
CCTTTACCTA	CACACTGGGG	ATTTGACCTC	TATCTCCACT	CTCATTAATA	TGGGTGGCCT	960
ATTTGCTCTT	ATTAAAAGGA	AAGGGGGAGA	TGTTGGGAGC	CGCGCCCA	TTCCGCTTGA	1020
CAAGATGGCG	CTGACAGCTG	TGTTCTAAGT	GGTAAACAAA	TAATCTGCGC	ATGCGCCGAG	1080
GGTGGTTCTT	CACTCCATGT	GCTCTGCCTT	CCCCGTGACG	TCAACTCGGC	CGATGGGCTG	1140
CAGTCAATCA	GGGAGTGACA	CGTCCTAGGC	GAAGGAAAT	TCTCCTTAAT	AGGGACGGGG	1200

TTTCGTTTTTC	TCTCTCTCTT	GCTTCGCTCT	CTCTTGCTTC	TTGCTCTCTT	TTCTGAAGA	1260
TGTAAGAATA	AAGCTTTGCC	GCAGAAGATT	CTGGTCTGTG	GTGTTCTTCC	TGGCCGCTCG	1320
TGAGAACGCG	TCTAATAACA	ATTGGTGCCG	AAACCCGGGT	GATAATGATT	ATCATCTACA	1380
TATCACAACG	TGCGTGGAGG					1400

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCTCCACGCA	CGTTGTGATA	TGTAGATGAT	AATCATTATC	ACTTTACGGG	TCCTTTCACT	60
ACAACCTGCCA	CGAGGCCCCCG	TGCTCTGGTA	ATAGATCTTT	GCTGAAAAGG	CACACACATG	120
ACACATTACT	CAAGGTGGGC	TCATCTGAGC	TGCAGATTCA	GCTTAATATG	AATCTTGCCA	180
ATTGTGTGAA	ATCATAAATC	TTCAAAGTGA	CACCTATTGC	CAGACACAGG	TGCCCCACCTT	240
TGGCATAATA	AACAAACACA	AATTATCTAT	TATATAAAGG	GTGTTAGAAG	ATGCTTTAGA	300
ATACAAATAA	ATCATGGTAG	ATAACAGTAA	GTTGAGAGCT	TAAATTTAAT	AAAGTGATAT	360
ACCTAATAAA	AATTAAATTA	AGAAGGTGTG	AATATACTAC	AGTAGGTAAA	TTATTTTCATT	420
AATTTATTTT	CTTCTTTAAT	CCTTTATAAT	GTTTTCTGCT	ATTGTCAATT	GCACATCCAT	480
ATGTTCAATT	CTTCACTGTA	ATGAAGAAAT	GTAGTAAATA	TACTTTCCGA	ACAAGTTGTA	540
TCAAATATGT	TACACTTGAT	TCCGTGTGTT	ACTTATCATT	TTATTATTAT	ATTGATTGCA	600
TTCTTTCGTT	ACTTGATATT	ATTACAAGGT	ACATATTTAT	TCTCTCAGAT	CTTCATTATA	660
CTCTAACCAT	TTTATAACAT	ACTTTATTTA	TTCAATTTCTT	ATGTGTGCTG	TGAGGCACAA	720
ATGCCAGAGA	GAACCTTGAGC	AGATAAGAGG	ACAAATTGCA	AGAGTCAGTT	ACCTCCTGCT	780
GTTCTTGGA	AACTCAGGAT	CAAATTCAGG	TTGTCAGGCT	TGGCAGCATG	CACTTTTTTAC	840
CAGTGCCCTCC	ATCTTGCTAG	CCCTGAACAT	CAAGCTTTGC	AGACAGACAG	GCTACACTAA	900
GTGAACTGGT	CATTACAGC	ATGCATGGTG	A'TTTATTGTT	ACTTTCTATT	CCATGCCTTT	960
ACTATTTCTA	CTAGGTGCTA	GCTAGTACTG	TATTTTCGAGA	TAGAAGTTAC	TGAAAGAAAA	1020
TTACATTGTT	TTCTATAGAT	CCTTGATACT	C'TTTCAGCAG	ATATAGAGTT	TTAATCAGGT	1080
CCTAGACCTT	TTCTTCACTC	TTATTAAATA	CTAAGTACAA	ATTAAGTTTA	TCCAAAACAG	1140
TACGGATGTT	GATTTTGTGC	AGTTCTACTA	TGATAATAGT	CTAGCTTCAT	AAATCTGACA	1200
CACCTATTGG	GAATGTTTTT	GTTAATAAAA	GATTCAGGTG	TTACTCTAGG	TCAAGAGAAT	1260
ATTAAACATC	AGTCCCAAAT	TACAAACTTC	AATAAAAGAT	TTGACTCTCC	AGTGGTGCCA	1320
ATATAAAGTG	ATAATGATTA	TCATCTACAT	ATCACAACGT	GCGTGGAGG		1369

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22118 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GAATTCCCTT	ATCCCTAATC	CAGATTGGTG	GAATAACTTG	GTATAGATGT	TTGTGCATTA	60
AAAACCCTGT	AGGATCTTCA	CTCTAGGTCA	CTGTTCAGCA	CTGGAACCTG	AATTGTGGCC	120
CTGAGTGATA	GGTCCTGGGA	CATATGCAGT	TCTGCACAGA	CAGACAGACA	GACAGACAGA	180
CAGACAGACA	GACAGACGTT	ACAAACAAAC	ACGTTGAGCC	GTGTGCCAAC	ACACACACAA	240
ACACCAGCTC	GGCCATAATT	ATTGAGGACG	TTGATTTATT	ATTCTGTGTT	TGTGAGTCTG	300
TCTGTCTGTC	TGTCTGTCTG	TCTGTCTGTC	TATCAAACCA	AAAGAAACCA	AACAATTATG	360

CCTGCCTGCC TGCCTGCCTG CCTACACAGA GAAATGATTT CTTCAATCAA TCTAAAACGA 420
 CCTCCTAAGT TTGCCTTTTT TCTCTTTCTT TATCTTTTTT TTTTCTTTT TCTTCTTCCT 480
 TCCTTCCTTC CTTCTTCCTT TCCTTCCTTT CTTTCTTTCT TTCTTTCTTT CTTACTTTCT 540
 TTCTTTCTCT CTTACATTTA TTCTTTTCAT ACATAGTTTC TTAGTGTAAG CATCCCTGAC 600
 TGTCTTGAAG ACACCTTTGT GGCCTCAATC CTGTAAGAGC CTTCCTCTGC TTTTCAAATG 660
 CTGGCATGAA TGTGTACCT CACTATGACC AGCTTAGTCT TCAAGTCTGA GTTACTGGAA 720
 AGGAGTTCCA AGAAGACTGG TTATATTTTT CATTTATTAT TGCATTTTAA TTAATAATTTA 780
 ATTTCCACAA AAGAATTTAG ACTGACCAAT TCAGAGTCTG CCGTTTAAAA GCATAAGGAA 840
 AAAGTAGGAG AAAAACGTGA GGCTGTCTGT GGATGGTCGA GGCTGCTTTA GGGAGCCTCG 900
 TCACCATTCT GCACTTGCAA ACCGGGCCAC TAGAACCCGG TGAAGGGAGA AACCAAAGCG 960
 ACCTGGAAAC AATAGGTCAC ATGAAGGCCA GCCACCTCCA TCTTGTGTG CGGGAGTTCA 1020
 GTTAGCAGAC AAGATGGCTG CCATGCACAT GTTGTCTTTC AGCTTGGTGA GGTCAAAGTA 1080
 CAACCGAGTC ACAGAACAAG GAAGTATACA CAGTGAGTTC CAGGTCAGCC AGAGTTTACA 1140
 CAGAGAAACC ACATCTTGAA AAAAACAAAA AAATAAATTA AATAAATATA ATTTAAAAAT 1200
 TTAATAATAG CCGGAGTGA TGGCGCATGT CTTAATCCG AGCTCTCTTC AGGCAGAGAT 1260
 GGGAGGATTT CTGAGTTTGA GGCCAGCCTG GTCTGCAAG TGAGTTCCAG GACAGTCAGG 1320
 GCTATACAGA GAAACCCTGT CTTGAAAACT AAATAAAT AAATAAAT AAATAAAT 1380
 AATATAAAT AAAAATTTTA AAGAATTTTA AAAAATAACA GAAATCAAAC ATAAGCCCAC 1440
 GAGATGGCAA GTAAGTCAA TCATAGCAGA AATATTATAC ACACACACAC ACACAGACTC 1500
 TGTATATAAA TCCAATGTGC CTTATGATG ATCAAGATTC CATAGTCAGT AATACTAGAA 1560
 GAATCATATG TCTGAAAATA AAAGCCAGAA CTTTCTCTGC TTTTGTCTTC TTTTGCCCCA 1620
 AGATAGGGTT TCTCTCAGTG TATCCCTGGC ATCCCTGCCT GGAACCTCCT TTGTAGGTTT 1680
 GGTAGCCTCA AACTCAGAGA GGTCTCTCTT GCCTGCCTGC CTGCCTGCCT GCCTGCCTGC 1740
 CTGCCCTGCC GCTGCCTCA CTTCTTCTCT CACCCACACA ACCGAGTCGA ACCTAGGATC 1800
 TTTATTTCTT TCTCTTTCTC TCTTCTTTCT TTCTTCTTTT CTTTCTTTCT TTCTTCTTTT 1860
 CTTTCTTTCT TTCTTATTCA ATTAGTTTTT AATGTAAGTG TGTGTTTGTG CTCTATCTGC 1920
 TGCCTATAGG CCTGCTTGCC AGGAGAGGGC AACAGAACCT AGGAGAAACC ACCATGCAGC 1980
 TCCTGAGAAAT AAGTGAAGAA ACAACAAAAA AAGGAAATTC TAATCACATA GAATGTAGAT 2040
 ATATGCCGAG GCTGTACAG TGCTTTTTAA GGCTTAGTGT AAGTAATGAA AATTGTTGTG 2100
 TGTCTTTTAT CCAAACACAG AAGAGAGGTG GCTCGGCCTG CATGTCTGTT GTCTGCATGT 2160
 AGACCAGGCT GGCCTTGAAC ACATTAATCT GTCTGCCTCT GCTTCCCTAA TGCTGCGATT 2220
 AAAGGCATGT GCCACCACTG CCCGGACTGA TTTCTTCTTT TTTTCTTTT TGGAAAAATAC 2280
 CTTTCTTTCT TTTTCTCTCT CTCTTTCTCT CTTCTCTCTT TTCTTTCTAT TCTTTTTTTC 2340
 TTTCTTTTTT CTTTTTTTTT TTTTTTTTTT AATTTGCCTA AGGTTAAAGG GTGCTCCAC 2400
 AATTGCCTCA GCTCTGCTCT AATTTCTCTT AAAAAAAAC AAACAAAAAA AAAACAAAAA 2460
 CAGTATGTAT GTATGTATAT TTAGAAGAAA TACTAATCCA TTAATAACTC TTTTTCCTA 2520
 AAATTCATGT CATTCTTGTT CCACAAAGTG AGTTCCAGGA CTTACCAGAG AAACCTGTG 2580
 TTCAAATTTG TGTGTTCAAG GTCACCTGG CTTACAAAGT GAGTTCCAAG TCCGATAGGG 2640
 CTACACAGAA AAACCATATC TCAGAAAAAA AAACACACAC AAACACACAC ACACACACAC 2700
 ACACACACAC ACACACACAC ACACACACAC ACACACACAG CGCGCCGCGG CGATGAGGGG 2760
 AAGTCGTGCC TAAAAATAAT ATTTTCTCTG CCAAAGTGAA AGCAAATCAC TATGAAGAGG 2820
 TACTCCTAGA AAAAATAAAT ACAAACGGGC TTTTAAATCA TTCCAGCACT GTTTTAAATT 2880
 AACTCTGAAT TTAGTCTTGG AAAAGGGGGC GGGTGTGGGT GAGTGAGGGC GAGCGAGCAG 2940
 ACGGGCGGGC GGGCGGGTGA GTGGCCGGCG CGGGTGGCAG CGAGCACCAG AAAACAACAA 3000
 ACCCAAGCG GTAGAGTGTT TTAATAATGA GACCTAAATG TGGTGGAACG GAGGTGCGCG 3060
 CCACCCTCCT CTTCCTCTGC TTAGATGCTC CTTTCCCTTT ACTGTGCTCC CTTCCCTTAA 3120
 CTGTGCCTAA CTGTGCCTGT TCCCTCACCC CGCTGATTCG CCAGCGACGT ACTTTGACTT 3180
 CAGAACGAT TTTGCTTGG TTTGCCCTGT CTTGCTCATC TTTCTGTTTT GGGTGCCCGA 3240
 GTCTAGCCCG TTCGCTATGT TCGGGCGGGA CGATGGGGAC CGTTTGTGCC ACTCGGGAGA 3300
 AGTGGTGGGT GGTACGCTG CTCCGTCTGT CGTGCGTGAG TGCCGGAACC TGAGCTCGGG 3360
 AGACCCTCCG GAGAGACAGA ATGAGTGAGT GAATGTGGCG GCGCGTGACG GATCTGTATT 3420
 GGTGTGTATG GTTGATCGAG ACCATTGTCT GGCACACCT AGTGGTGACA AGTTTCGGGA 3480
 ACGCTCCAGG CCTCTCAGT TGGTGACACA GGAGAGGGAA GTGCCCTGTGG TGAGGCGACC 3540
 AGGGTGACAG GAGGCCGGGC AAGCAGGCGG GAGCGTCTCG GAGATGGTGT CGTGTTTAAAG 3600
 GACGGTCTCT AACAAAGAGG TCGTACAGGG AGATGGCCAA AGCAGACCGA GTTGCTGTAC 3660
 GCCCTTTTGG GAAAAATGCT AGGGTTGGTG GCAACGTTAC TAGGTCGACC AGAAGGCTTA 3720
 AGTCCTACCC CCCCCCCCCC TTTTCTTTT TTTCTTCCAG AAGCCCTCTC TTGTCCCCGT 3780
 CACCGGGGGC ACCGTACATC TGAGGCCGAG ATGACCGGAT GGGCCCCGGT TCCAAGCCGG 3840
 TGTGGCTCGG CCAGCTGGCG CTTGCGGTCT TTTTCTTTT TTTTCTTTT TTTTCTCTCA 3900
 GAAGCCTTGT CTGTGCTGT CACCGGGGGC GCTGTACTTC TGAGGCCGAG AGGACGCGAT 3960
 GGGCCCCGGC TTCCAAGCCG GTGTGGCTCG GCCAGCTGGA GCTTCGGGTC TTTTCTTTT 4020
 TTTTCTTTT CAGAAGCCTT CTTGCTCGCT GTACCCGGG GTCACCGGG GCGCTGTACT 4080
 TCTGAGGCCG AGAGGACGCG ATGGGTGCGC TTCCAAGCCG ATGTGGCGGG GCCAGCTGGA 4140
 GCTTCGGGTT TTTTCTTTT CTCCAGAAGC CCTCTCTTGT CCCCCTCACC GGGGGCGCTG 4200
 TACTTCTGAG GCCGAGAGGA CGTGATGGGC CCGGGTTCCA GCGCGATGTC GCCCGGTCAG 4260
 CTGAGCTTTT GGATCTTTT TTTTCTTTT CCTCCAGAAG CCCTCTCTTG TCCCCGTCAC 4320
 CGGGGGCACC TTACATCTGA GGGCGAGAGG ACGTGATGGG TCCGGCTTCC AAGCCGATGT 4380

GGCGGGGCCA GCTGGAGCTT CGGGTTTTTT TTTTTCCTC CAGAAGCCCT CTCTTGTCCT 4440
CGTCACCGGG GCGCTGTAC TTCTGAGGCC GAGAGGACGT GATGGGCCCG GGTTCAGGC 4500
GGATGTCGCC CGGTACAGTG GAGCTTTGGA TCATTTTTTT TTTTCCCTCC AGAAGCCCTC 4560
TCTTGTCCTCC GTCACCGGGG GCACCGTACA TCTGAGGCCG AGAGGACACG ATGGGCCTGT 4620
CTTCCAAGCC GATGTGGCCC GGCCAGCTGG AGCTTCGGGT CTTTTTTTTT TTTTTCTCTC 4680
CAGAAGCCTT GTCTGTCGCT GTACCCCGGG GCGCTGTACT TCTGAGGCCG AGAGGACGCG 4740
ATGGGCCCGG CTTCCAAGCC GGTGTGGCTC GGCCAGCTGG AGCTTCGGGT CTTTTTTTTT 4800
TTTTTTTTTT TTCTCCAGA AACCTTGTCT GTCGTGTCA CCCGGGGCGC TTGTACTTCT 4860
GATGCCGAGA GGACGCGATG GGCCCGTCTT CCAGGCCGAT GTGGCCCGGT CAGCTGGAGC 4920
TTTGGATCTT TTTTTTTTTT TTTTCTCCA GAAGCCCTCT CTTGTCCCCG TCACCGGGGG 4980
CACCTTACAT CTGAGGCTA GAGGACACGA TGGGCCCGGG TTCCAGGCCG ATGTGGCCCG 5040
GTCAGCTGGA GCTTTGGATC TTTTTTTTTT TTTTCTTCCA GAAGCCCTCT TGTCCCCGTC 5100
ACCGGTGGCA CTGTACATCT GAGGCGGAGA GGACATTATG GGCCCGGCTT CCAATCCGAT 5160
GTGGCCCGGT CAGCTGGAGC TTTGGATCTT ATTTTTTTTT TAATTTTTTC TTCCAGAAGC 5220
CCTCTTGTC CTGTACCGG TGGCACGGTA CATCTGAGGC CGAGAGGACA TTATGGGCC 5280
GGCTTCCAGG CCGATGTGGC CCGGTCACTT GGAGCTTTGG ATCTTTTTTT TTTTTTTTCT 5340
TTTTTCTCTC AGAAGCCCTC TCTGTCCCTG TCACCGGGGG CCCTGTACGT CTGAGGCCGA 5400
GGGAAAGCTA TGGGCGCGGT TTTCTTTTCT TGACCTGTCT GTCTTATCAG TTCTCCGGGT 5460
TGTGAGGCT GACCAGTTGT TCCTTTGAGG TCCGGTCTCT TTCGTTATGG GGTCAATTTT 5520
GGGCCACCTC ACTTCCAGGC GCTGTTGCTC GCCTGTCACT TTCTCCCTGT 5580
TCTCTTTTAT GCTTGTGATC TTTTCTATCT GTTCTATTG GACCTGGAGA TAGGTACTGA 5640
CACGCTGTCC TTTCCCTATT AACACTAAAG GACACTATAA AGAGACCCTT TCGATTTAAG 5700
GCTGTTTTGC TTGTCCAGCC TATTCTTTTT ACTGGCTTGG GTCTGTGCGG GTGCCTGAAG 5760
CTGTCCCCGA GCCACGCTTC CTGCTTTTCC GGGCTTGCTG CTTGCGTGTG CTTGCTGTGG 5820
GCAGCTTGTG ACAACTGGGC GCTGTGACTT TGCTGCTGT CAGACGTTTT TCCCGATTTC 5880
CCCGAGGTGT CGTTGTCACA CCTGTCCCGG TTGGAATGGT GGAGCCAGCT GTGGTTGAGG 5940
GCCACCTTAT TTCGGCTCAC TTTTTTTTTT TTTTTTCTC TTGGAGTCCC GAACCTCCGC 6000
TCTTTTCTCT TCCCGGTCTT TCTTCCACAT GCCTCCCGAG TGCATTTCTT TTTGTTTTTT 6060
TTCTTTTTTT TTTTTTTTTT TTGGGAGGT GGAGAGTCCC GAGTACTTCA CTCCTGTCTG 6120
TGGTGTCCAA GTGTTTATGC CACGTGCTC CCGAGTGCAC TTTTTTTGT TTTTTTTGT GGCAGTCGCT 6180
CGTTGTGTTT TCTTGTCTG TGTCTGCCCC TATCAGTAAC TGTCTTGCCC CGCGTGTAA 6240
ACATTCCCTAT CTCGCTTGTG TCTCCCGATT GCGCGTCGTT GCTCACTCTT AGATCGATGT 6300
GGTGCTCCGG AGTTCTCTTC GGGCCAGGGC CAAGCCGCGC CAGGCGAGGG ACGGACATT 6360
ATGGCGAATG CCGGCGCTC TTCTGTTCT CCGAGCGGGC CCTCGTCTCT CCACCCATC 6420
CGTCTGCCGG TGGTGTGTGG AAGGCAGGGG TGCGGCTCTC CGGCCCCGAC CTGCCCCGCG 6480
CGCACTTTTC TCAGTGGTTC GCGTGGTCT TGTGGATGTG TGAGGCGCCC GGTGTGTGCC 6540
TCACGTGTTT CACTTTGGTC GTGTCTCGCT TGACCATGTT CCCAGAGTCG GTGGATGTGG 6600
CCGTGGCGCT TGCATACCCT TCCCGTCTGG TGTGTGCACG CGCTGTTTCT TGTAAAGCTC 6660
GAGGTGCTCC TGGAGCGTTC CAGGTTTGTC TCCTAGGTGC CTGCTTCTGA CTTGGTGGTG 6720
GCGCTCCCCA TTCCCTGGTG TGCCTCCGGT GCTCCGCTCTG GCTGTGTGCC TTCCCGTTTG 6780
TGTCTGAGAA GCGCGTGAGA GGGGGTCTGA GGAGAGAAGG AGGGGCAAGA CCCCCCTTCT 6840
TCGTCCGGTG AGGCGCCAC CCCGCGACTA GTACGCTGT GCGTAGGGCT GGTGTGAGC 6900
GGTCGCGGCT GGGTTGGAA AGTTTCTCGA GAGACTCAT GCTTTCCCGT GGGGAGCTTT 6960
GAGAGGCCCT GCTTTCCGGG GGGACCGGTT GCAGGCTCTC CCTGTCCCG GGATGCTCAG 7020
AATGCCCTTG GAAGAGAACC TTCCTGTTGC CGCAGACCCC CCCGCGCGGT CGCCGCGCTG 7080
TTGGTCTTCT GGTTTCCCTG TGTGCTCGTC GCATGCATCC TCTCTCGGTG GCCGGGGCTC 7140
GTCGGGGTTT TGGGTCCGTC CCGCCCTCAG TGAGAAAGTT TCCTTCTCTA GCTATCTTCC 7200
GGAAAGGGTG CCGGCTTCTT ACGGTCTCGA CCGGTCTCTC CCGAATGGT CCGTGGAGG 7260
CTCGCCCCCT GACCGCTCC CGCGCGCGCA GCGTTTGCTC TCTCGTCTAC CGCGGCCGCG 7320
GGCCTCCCCG CTCCGAGTTC GGGGAGGGAT CACGCGGGG AGAGCCTGTC TGTGCTCCTG 7380
CCGTGTGCTG GGAGCATGTG GCTCGGCTTG TGTGGTTGGT GGCTGGGGAG AGGGCTCCGT 7440
GCACACCCCC GCGTGCGCT ACTTCTCTCC CCTCTGAGG GCCGCCGTG GGACGGGGTG 7500
TGGGTAGGCG ACGGTGGGCT CCCGGTCCC CACCCGTCTT CCGTGCCTC ACCCGTCCCT 7560
TCCGTGCGCT GCGTCCCTCT CGCTCGCGTC CACGACTTTG GCCGCTCCCC CGACGGCGGC 7620
CTGCGCCGCG CGTGGTGCCT GCTGTGTGCT TCTCGGGCTG TGTGGTTGTG TCGCCTCGCC 7680
CCCCCTTCC CGCGGCAGCG TTCCACGGC TGGCGAAATC GCGGGAGTCC TCCTTCCCT 7740
CCTCGGGGTG GAGAGGGTCC GTGTCTGGC TTGATTGATC TCGTCTCGG GGACGGGACC 7800
GTTCTGTGGG AGAACGGCTG TTGGCCCGCT CCGGCGCGAC GTCGGACGTG GGGACCCACT 7860
GCCGCTCGGG GGTCTTCGTC GGTAGGCATC GGTGTGTGCG CATCGGTCTC TCTCTCGTGT 7920
CGGTGTGCGC TCCTCGGGCT CCCGGGGGGC CGTGTGTTT CCGGTGCGGT CGGCGCTGCA 7980
GGTGTGGTGT GACTGCTCAG GGGAGTGGT CAGTGTGATT CCCGCCGTT TTGCTCGCG 8040
TGCCCTGACC GGTCCGACGC CCGAGCGGTC TCTCGTCCC TTGTGAGGAC CCCCTCCCG 8100
GAGGGGCCCG TTTCCGGCCG CCTTGCCGTC GTCGCCGGCC CTCGTTCTGC TGTGTGTTT 8160
CCCCCTCCCC GCTCGCCGCA GCCGGTCTTT TTTCTCTCT CCCCCCTCT CCTCTGACTG 8220
ACCCGTGGCC GTGCTGTGCG ACCCCCCGAG TGGGGGCGCG CGGGCACGTA CGCGTCCGGG 8280
CGGTACCGG GGTCTTGGGG GGGGGCCGAG GGGTAAGAAA GTCGGCTCGG CGGGCGGAG 8340
GAGCTGTGGT TTGGAGGCG TCCCGGCCCC GCGGCCGTG CGGTGTCTTG CGCGTCTTG 8400

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GAGAGGGCTG	CGTGCGAGGG	GAAAAGGTTG	CCCCGCGAGG	GCAAAGGGAA	AGAGGCTAGC	8460
AGTGGTCATT	GTCCCCACGG	TGTGGTGGTC	TGTTGGCCGA	GGTGCCTCTG	GGGGGCTCGT	8520
CCGGCCCTGT	CGTCCGTCGG	GAAGGCGCGT	GTTGGGGCCT	GCCGGAGTGC	CGAGGTGGGT	8580
ACCCTGGCGG	TGGGATTAAC	CCCGCGCGCG	TGTCCCGGTG	TGGCGGTGGG	GGCTCCGGTC	8640
GATGTCTACC	TCCCTCTCCC	CGAGGTCTCA	GGCCTTCTCC	GCGCGGGCTC	TCGGCCCTCC	8700
CCTCGTTCCT	CCCTCTCGCG	GGGTTCAGT	CGCTCGTCGA	CCTCCCCCTC	TCCGTCCTTC	8760
CATCTCTCGC	GCAATGGCGC	CGCCCGAGTT	CACGGTGGGT	TCGTCTCTCC	CCTCCGCTTC	8820
TCGCCGGGGG	CTGGCCGCTG	TCCGGTCTCT	CCTGCCCGAC	CCCCGTGTCG	GTGGTCTTCT	8880
CTCGCCGGCT	TCGCGGACTC	CTGGCTTCGC	CCGGAGGGTC	AGGGGGCTTC	CCGGTTCCTCC	8940
GACGTTGCGC	CTCGCTGCTG	TGTGCTTGGG	GGGGGCCCCG	TGCGGCCTCC	GCCCGCCCGT	9000
GAGCCCCCTG	CGCACCCGCC	GGTGTGCGGT	TTCGCGCCGC	GGTCAGTTGG	GCCCTGGCGT	9060
TGTGTGCGCT	CGGGAGCGTG	TCCGCCTCGC	GGCGGCTAGA	CGCGGGTGTC	GCCGGGCTCC	9120
GACGGGTGGC	CTATCCAGGG	CTCGCCCCCG	CCGACCCCCG	CCTGCCCGTC	CCGGTGGTGG	9180
TCGTTGGTGT	GGGGAGTGAA	TGGTGCTACC	GGTCATTCCC	TCCCGCGTGG	TTTGACTGTC	9240
TCGCCGGTGT	CGCGCTTCTC	TTTCCGCCAA	CCCCACGCC	AACCCACCAC	CCTGCTCTCC	9300
CGGCCCGGTG	CGGTTCGACGT	TCCGGCTCTC	CCGATGCCGA	GGGGTTCGGG	ATTTGTGCCG	9360
GGGACGGAGG	GGAGAGCGGG	TAAGAGAGGT	GTCCGAGAGC	TGTCCCGGGG	CGACGCTCGG	9420
GTTGGCTTTG	CCGCGTGCGT	GTGCTCGCGG	ACGGGTTTTG	TCGGACCCCG	ACGGGGTCGG	9480
TCCGGCCCGA	TGCACTCTCC	CGTTCGCGCG	GAGCGCCCCG	CCGGCTCACC	CCCGGTTTGT	9540
CCTCCCGCGA	GGCTCTCCGC	CGCCGCCCGC	TCCTCTCTCT	CTCTCGCGCT	CTCTGTCCCG	9600
CCTGGTCCTG	TCCCACCCCC	GACGCTCCGC	TCGCGCTTCC	TTACCTGGTT	GATCCTGCCA	9660
GGTAGCATAT	GCTTGTCTCA	AAGATTAAGC	CATGCATGTC	TAAGTACGCA	CGGCCGGTAC	9720
AGTGAAACTG	CGAATGGCTC	ATTAAATCAG	TTATGGTTCC	TTTGGTCGCT	CGTCTCTCTC	9780
CTACTTGGAT	AACGTGTGGTA	ATTCTAGAGC	TAATACATCC	CGACGGGCGC	TGACCCCCCT	9840
TCCCGGGGGG	GGATGCGTGC	ATTTATCAGA	TCAAAACCAA	CCCGGTGAGC	TCCCTCCCGG	9900
CTCCGGCCCG	GGGTGCGGCG	CCGGCGGCTT	GGTGA CTCTA	GATAACCTCG	GGCCGATCGC	9960
ACGCCCCCGG	TGGCGGCGAC	GACCCATTCC	AACGTCTGCC	CTATCAACTT	TCGATGGTAG	10020
TCGCCGTGCC	TACCATGGTG	ACCACGGGTG	ACGGGGAATC	AGGGTTCGAT	TCCGGAGAGG	10080
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GGAATGAGTC	CACTTTAAAT	CCTTTAACGA	GGATCCATTG	GAGGGCAAGT	CTGGTGCCAG	10260
CAGCCGCGGT	AATTCCAGCT	CCAATAGCGT	ATATTAAAGT	TGCTGCAGTT	AAAAAGCTCG	10320
TAGTTGGATC	TTGGGAGCGG	GCGGGCGGCT	CGCCGCGAGG	CGAGTCACCG	CCCGTCCCCG	10380
CCCTTGCCCT	CTCGGCGCCC	CCTCGATGCT	CTTAGCTGAG	TGTCCCGCGG	GGCCCGAAGC	10440
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GCAAGACGGA	CCAGAGCGAA	AGCATTTCGC	AAGAATGTTT	TCATTAATCA	AGAACGAAAG	10680
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CACGTGTCTC	GTTTCGTTCC	TGCTGGCCCG	CCTGAGGCTA	CCCCCTCGGTC	CATCTGTTCT	12420

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(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 42999 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

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GCAGAGACGC	GTTTTGGGCA	CCGTTTGTGT	GGGTTTGGGG	CAGAGGGGCT	GCCTTTTTCGG	42000
CCTCGGGAAG	AGCTTCTCGA	CTCACGGTTT	CGCTTTCGCG	GTCCACGGGC	CGCCCTGCCA	42060
GCCGATCTG	TCTCGCTGAC	GTCCGCGGCG	GTTGTCGGGC	TCCATCTGGC	GGCCGCTTTG	42120
AGATCGTGCT	CTCGGCTTCC	GGAGCTGCGG	TGGCAGCTGC	CGAGGGAGGG	GACCGTCCCC	42180
GCTGTGAGCT	AGGCAGAGCT	CCGGAAGGCC	CGCGGTCGTC	AGCCCCGGCTG	GCCCCGTGGC	42240
GCCAGAGCTG	TGGCCGGTCG	CTTGTGAGTC	ACAGCTCTGG	CGTGCAGGTT	TATGTGGGGG	42300
AGAGGCTGTC	GCTGCGCTTC	TGGGCCCGCG	GCGGGCGTGG	GGCTGCCCGG	GCCGGTCGAC	42360
CAGCGCGCCG	TAGCTCCCCA	GGCCCCGCGC	GCGACCCGGC	GGACCCGCGG	CGCGTGGCGG	42420
AGGCTGGGGA	CGCCCTTCCC	GGCCCCGGTC	CGGTCCGCTC	ATCCTGGCCG	TCTGAGGCGG	42480
CGGCCGAATT	CGTTTCCGAG	ATCCCCGTGG	GGAGCCGGGG	ACCGTCCCGC	CCCCGTCCCC	42540
CGGGTGCCGG	GGAGCGGTCC	CCGGGCCGGG	CCGCGGTCCC	TCTGCCGCGA	TCCTTTCTGG	42600
CGAGTCCCCG	TGGCCAGTCG	GAGAGCGCTC	CCTGAGCCGG	TGCGGCCCGA	GAGGTCGCGC	42660
TGGCCGGCCT	TCGGTCCCTC	GTGTGTCCCG	GTCTAGGAG	GGGCCGGCCG	AAAATGCTTC	42720
CGGCTCCCGC	TCTGGAGACA	CGGGCCGGCC	CCTGCGTGTG	GCCAGGGCGG	CCGGGAGGGC	42780
TCCCCGGCCC	GGCGCTGTCC	CCGCGTGTGT	CCTTGGGTTG	ACCAGAGGGA	CCCCGGGCGC	42840
TCCGTGTGTG	GCTGCGATGG	TGGCGTTTTT	GGGGACAGGT	GTCCGTGTCC	GTGTCGCGCG	42900
TCGCCTGGGC	CGGCGGCGTG	GTCCGTGACG	CGACCTCCCC	GCCCCGGGGG	AGGTATATCT	42960
TTCGCTCCGA	GTCCGCAATT	TTGGGCCGCC	GGGTTATAT			42999

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTCCCCGCGG	GCCCCCGTGT	TCGCCGTTCC	CGTGGCGCGG	ACAATGCGGT	TGTGCGTCCA	60
CGTGTGCGTG	TCCGTGCAGT	GCCGTTGTGG	AGTGCCTCGC	TCTCCTCCTC	CTCCCCGGCA	120
GCGTTCCAC	GGTTGGGGAC	CACCGGTGAC	CTCGCCCTCT	TGGGGCCTGG	ATCCG	175

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 755 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
 (iii) HYPOTHETICAL: NO
 (iv) ANTISENSE: NO
 (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTCTGGTGG	GAATTGTTGA	CCTCGCTCTC	GGGTGCGGCC	TTTGGGGAAC	GGCGGGGTCG	60
GTCGTGCCCC	GCGCCGGACG	TGTGTCGGGG	CCCCTTCCCT	GCTCGAGGGT	GGCGGTGGCG	120
GCGGCGTTGG	TAGTCTCCCG	TGTTGCGTCT	TCCCGGGCTC	TTGGGGGGGG	TGCCGTGCTT	180
TTCCGGGGCCG	GCGTTGCTTG	GCTTACGCAG	GCTTGGTTTTG	GGACTGCCTC	AGGAGTCGTG	240

GGCGGTGTGA	TTCCCGCCGG	TTTTGCCTCG	CGTCTGCCTG	CTTTGCCTCG	GGTTTGCTTG	300
GTTCGTGTCT	CGGGAGCGGT	GGTTTTTTTT	TTTTTCGGGT	CCCCGGGAGA	GGGGTTTTTC	360
CGGGGGACGT	TCCCGTCGCC	CCCTGCCGCC	GGTGGGTTTT	CGTTTCGGGC	TGTGTTCGTT	420
TCCCCTTCCC	CGTTTCGCCG	TCGGTTCTCC	CCGGTCGGTC	GGCCCTCTCC	CCGGTCGGTC	480
GCCCGGCCGT	GCTGCCGGAC	CCCCCTTCT	GGGGGGGATG	CCCCGGGCACG	CACGCGTCCG	540
GGCGGCCACT	GTGGTCCGGG	AGCTGCTCGG	CAGGCGGGTG	AGCCAGTTGG	AGGGGCGTCA	600
TGCCCCCGCG	GGCTCCCGTG	GCCGACGCGG	CGTGTTCCTT	GGGGGGGCCT	GTGCGTGC GG	660
GAAGGCTGCG	CACGTTGTCG	GTCCTTGCGA	GGGAAAGAGG	CTTTTTTTTT	TTAGGGGGTC	720
GTCCTTCGTC	GTCCCGTCGG	CGGTGGATCC	GGCCT			755

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 463 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GGCCGAGGTG	CGTCTGCGGG	TTGGGGCTCG	TCCGGCCCCG	TCGTCTCCG	GGAAGGCGTT	60
TAGCGGTAC	CGTCGCCCGG	CCGAGGTGGG	CGCACGTCGG	TGAGATAACC	CCGAGCGTGT	120
TTCTGGTTGT	TGGCGGCGGG	GGCTCCGGTC	GATGTCTTCC	CCTCCCCCTC	TCCCCGAGGC	180
CAGGTCAGCC	TCCGCCTGTG	GGCTTCGTCG	GCCGTCTCCC	CCCCCTCAC	GTCCCTCGCG	240
AGCGAGCCCG	TCCGTTTCGAC	CTTCCTTCCG	CCTTCCCCCC	ATCTTCCCG	GCTCCGTTGG	300
CCCCGGGGTT	TTCACGGCGC	CCCCACGCT	CCTCCGCCTC	TCCGCCCGTG	GTTTGGACGC	360
CTGGTTCCGG	TCTCCCCGCC	AAACCCCGGT	TGGGTTGGTC	TCCGGCCCCG	GCTTGCTCTT	420
CGGCTCTCCC	AACCCCGGC	CGGAAGGGT	CGGGGGTTCC	GGG		463

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGATTCTTCA	GGATTGAAAC	CCAAACCGGT	TCAGTTTCTT	TTCCGGCTCC	GGCCGGGGGG	60
GGCGGCCCCG	GGCGGTTTGG	TGAGTTAGAT	AACCTCGGGC	CGATCGCACG	CCCCCGTGG	120
CGGCGACGAC	CCATTGGAAC	GTCTGCCCTA	TCAACTTTCG	ATGGTAGTCG	ATGTGCCTAC	180
CATGGTGACC	ACGGGTGACG	GGGAATCAGG	GTTCGATTCC	GGAGAGGGAG	CCTGAGAAAC	240
GGCTACCACA	TCCAAGGAAG	GCAGCAGGCG	CGCAAATTAC	CCACTCCCGA	CCCGGGGAGG	300
TAGTGACGAA	AAATAACAAT	ACAGGACTCT	TTGAGGCCCC	TGTAATTGGA	ATGAGTCCAC	360
TTTAAATCCT	TTAAGCAG					378

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 378 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATCCATTGG	AGGGCAAGTC	TGGTGCCAGC	AGCCGCGGTA	ATTCCAGCTC	CAATAGCGTA	60
TATTAAAGTT	GCTGCAGTTA	AAAAGCTCGT	AGTTGGATCT	TGGGAGCGGG	CGGGCGGTCC	120
GCCGCGAGGC	GAGTACCGC	CCGTCCCCCG	CCCTTGCCCTC	TCGGCGCCCC	CTCGATGCTC	180
TTAGCTGAGT	TGTCCCGCGG	GGCCCGAAGC	GTTTACTTTG	AAAAAATTAG	AGTTGTTTCA	240
AAGCAGGCC	GAGCCGCCTG	GATACCGCCA	GCTAGGAAAT	AATGGAATAG	GACCGCGGTT	300
CCTATTTTGT	TTGGTTTTTCG	GAAGTGAGCC	CATGATTAAG	GGAAACGGCC	GGGGGCATTC	360
CCTTATTGCG	CCCCCCTA					378

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 719 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

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GGATCTTTCC	CGCTCCCCGT	TCCTCCCGGC	CCCTCCACCC	GCGCGTCTCC	CCCCTTCTTT	60
TCCCCTCTCC	GGAGGGGGGG	GAGGTGGGGG	CGCGTGGGCG	GGGTGCGGGG	TGGGGTCGGC	120
GGGGGACCGC	CCCCGGCCGG	CAAAAGGCCG	CCGCCGGGCG	CACTTCAACC	GTAGCGGTGC	180
GCCGCGACCG	GCTACGAGAC	GGCTGGGAAG	GCCCCACGGG	GAATGTGGCT	CGGGGGGGGC	240
GGCGCGTCTC	AGGGCGCGCC	GAACCACCTC	ACCCCGAGTG	TTACAGCCCT	CCGGCCGCGC	300
TTTCGCGGAA	TCCCAGGGCC	GAGGGGAAGC	CCGATACCCG	TCGCCGCGCT	TTCCCCCTCC	360
CCCCGTCCGC	CTCCCGGGCG	GGCGTGGGGG	TGGGGGCGCG	GCCGCCCCCTC	CCACGCCCGT	420
GGTTTCTCTC	TCTCCCGGTC	TCGGCCGGTT	TGGGGGGGGG	AGCCCGGTTG	GGGGCGGGGC	480
GGACTGTCCT	CAGTGCGCC	CGGGCGTCGT	CGCGCCGTCG	GGCCCGGGGG	GTTCTCTCGG	540
TCACGCCGCC	CCCGACGAAG	CCGAGCGCAC	GGGGTCGGCG	GCGATGTCGG	CTACCCACCC	600
GACCCGCTTT	GAAACACGGA	CCAAGGAGTC	TAACGCGTGC	GCGAGTCAGG	GGCTCGCACG	660
AAAGCCGCCG	TGGCGCAATG	AAGGTGAAGG	GCCCCGTCCG	GGGGCCCGAG	GTGGGATCC	719

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 685 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGAGGCCTCT	CCAGTCCGCC	GAGGGCGCAC	CACCGGCCCG	TCTCGCCCGC	CGCGTCGGGG	60
AGGTGGAGCA	CGAGCGTACG	CGTTAGGACC	CGAAAGATGG	TGAACTATGC	CTGGGCAGGG	120
CGAAGCCAGA	GGAAACTCTG	GTGGAGGTCC	GTAGCGGTCC	TGACGTGCAA	ATCGGTGCTC	180
CGACCTGGGT	ATAGGGGCGA	AAGACTAATC	GAACCATCTA	GTAGCTGGTT	CCCTCCGAAG	240
TTTCCCTCAG	GATAGCTGGC	GCTCTCGCAA	CCTTCGGAAG	CAGTTTTATC	CGGGTAAAGG	300
CGGAATGGAT	TAGGAGGTCT	TGGGGCCGGA	AACGATCTCA	AACTATTTCT	CAAACTTTAA	360

ATGGGTAAGG	AAGCCCGGCT	CGCTGGCGTG	GAGCCGGGCG	TGGAATGCGA	GTGCCTAGTG	420
GGCCACTTTT	GGTAAGCAGA	ACTGGCGCTG	CGGGATGAAC	CGAACGCCGG	GTTAAGGCGC	480
CCGATGCCGA	CGCTCATCAG	ACCCAGAAAA	AGGTGTTGGT	TGATATAGAC	AGCAGGACGG	540
TGGCCATGGA	AGTCGGAATC	CGCTAAGGAG	TGTGTAACAA	CTCACCTGCC	GAATCAACTA	600
GCCCTGAAAA	TGGATGGCGC	TGGAGCGTCG	GGCCCATACC	CGGCCGTCGC	CGGCAGTCGG	660
AACGGGACGG	GACGGGAGCG	GCCGC				685

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GAGGAATTCC CCTATCCCTA ATCCAGATTG GTG 33

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 35 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AAACTGCAGG CCGAGCCACC TCTCTTCTGT GTTTG 35

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGGAATTCAC AGAAGAGAGG TGGCTCGGCC TGC 33

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGCCTGCAGG AAGTCATACC TGGGGAGGTG GCCC

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(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 80 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AAACTGCAGG TTAATTAACC CTAACCCTAA CCCTAACCTT AACCTTAACC CTAACCCTAA
CCCTAACCTT AACCCGGGAT

60
80

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TTGGGCCCTA GGCTTAAGG

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(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA
(iii) HYPOTHETICAL: NO
(iv) ANTISENSE: NO
(v) FRAGMENT TYPE:
(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGGGTTT TCCCAGTCAC GACGT

25

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTGCAAGGC GATTAAGTTG GGTAAC

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(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TATGTTGTGT GGAATTGTGA GCGGAT

26

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: Genomic DNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
- (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGGTTTAAAC AGATCTCTGC A

21